

## SEQUENCE LISTING

### (1) GENERAL INFORMATION:

(i) APPLICANT: ARATHOON, R.  
CARTER, P.J.  
MERCHANT, A.M.  
PRESTA, L.G.

(ii) TITLE OF INVENTION: METHOD FOR MAKING MULTISPECIFIC ANTIBODIES  
HAVING HETEROMULTIMERIC AND COMMON  
COMPONENTS

(iii) NUMBER OF SEQUENCES: 26

(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94080

(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: Unassigned  
(B) FILING DATE: 30-Apr-1998  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Conley, Deirdre L.  
(B) REGISTRATION NUMBER: 36,487  
(C) REFERENCE/DOCKET NUMBER: P1099R1

(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650/225-2066  
(B) TELEFAX: 650/952-9881

### (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCTTCCCGA GATGGGGGCA GGGTGCACAC CTGTGG 36

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTCTTCCCGA CATGGGGGCA G 21

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGTCATCTCA CACCGGGATG G 21

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CTTGGTCATA CATTACGGG ATGG 24

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CTCTTCCCGA GATGGGGGAC AGGTGTACAC 30

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GCCGTCGGAA CACAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGGAGTCT AGAACGGGAG GCGTGGTACA GTAGTTGTT 39

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTCGGAGTCT AGAACGGGAG GACAGGTCTT GTA 33

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCGGAGTCT AGACAGGGAG G 21

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GCCGTCGGAG CTCAGCACGG G 21

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGAGGCGTG GTGCTGTAGT TGTT 24

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

G TTCAGGTGC TGGGCTCGGT GGGCTTGTGT GAGTTTTG 38

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 821 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AACGCGTACG CTCTGAAAAT GCGCGACCCG AACCGTTTTTC GTGGTAAAGA 50  
TCTGGCTGCA CACTACGGCC AGCCGCGGGA ACCTCAGGTG TATACCCTGC 100  
CACCGTCTCG AGAAGAAATG ACTAAAAACC AGGTCTCTCT GTGGTGCCTG 150  
GTCAAAGGTT TCTATCCGAG CGATATCGCC GTGGAATGGG AAAGCAACGG 200  
TCAACCGGAA AACAACTACA AAACCACTCC ACCGGTGCTG GATTCTGATG 250  
GCTCCTTCTT TCTGTATTCG AAGCTGACCG TTGACAAAAG CCGTTGGCAG 300  
CAAGGCAACG TTTTCAGCTG TTCTGTTATG CACGAGGCCT TGCACAACCA 350  
CTACACCCAG AAAAGCCTGT CCCTGTCTCC CGGGAAATAA GCTGAGGCTC 400  
CTCTAGAGGT TGAGGTGATT TTATGAAAAA GAATATCGCA TTTCTTCTTG 450  
CATCTATGTT CGTTTTTTCT ATTGCTACAA ACGCGTACGC TGGGCAGCCC 500  
CGAGAACCAC AGGTGTACAC CCTGCCCCCA TCCCGGGAAG AGATGACCAA 550  
GAACCAGGTA AGCTTGTA CT GCCTGGTCAA AGGCTTCTAT CCCAGCGACA 600  
TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC 650  
ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCTTTCT 700  
CACCGTCGAC AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG 750  
TGATGCATGA GGCTCTGCAC AACCCTACA CGCAGAAGAG CCTCTCCCTG 800  
TCTCCGGGTA AATAGGGGCC C 821

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ser	Asn	Arg	Phe	Ser	Gly	Ser	Lys	Ser	Gly	Asn	Thr	Ala	Ser	Leu
1				5					10					15
Thr	Ile	Ser	Gly	Leu	Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys
				20					25					30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
 35 40 45

Lys Leu Thr Val Leu  
 50

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu  
 1 5 10 15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
 20 25 30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
 35 40 45

Lys Leu Thr Val Leu  
 50

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 50 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu  
 1 5 10 15

Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
 20 25 30

Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
 35 40 45

Lys Leu Thr Val Leu  
 50

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
 1              5              10              15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
              20              25              30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
              35              40              45
Lys Leu Thr Val Leu
              50
```

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu
 1              5              10              15
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys
              20              25              30
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr
              35              40              45
Lys Leu Thr Val Leu
              50
```

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Ser Thr Ala Ser Leu  
1 5 10 15  
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
20 25 30  
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
35 40 45  
Lys Leu Thr Val Leu  
50

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ser Asn Arg Phe Ser Gly Ser Lys Xaa Gly Asn Thr Ala Ser Leu  
1 5 10 15  
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
20 25 30  
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
35 40 45  
Lys Leu Thr Val Leu  
50

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu  
1 5 10 15  
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
20 25 30  
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
35 40 45



Lys Leu Thr Val Leu  
50

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 50 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Asn Arg Phe Ser Gly Ser Lys Ser Gly Asn Thr Ala Ser Leu  
1 5 10 15  
Thr Ile Ser Gly Leu Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys  
20 25 30  
Ser Ser Tyr Thr Thr Arg Ser Thr Arg Val Phe Gly Gly Gly Thr  
35 40 45  
Lys Leu Thr Val Leu  
50

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser  
1 5 10 15  
Lys Asn Thr Leu Tyr Leu Gln Met Asn Arg Leu Arg Ala Glu Asp  
20 25 30  
Thr Ala Val Tyr Tyr Cys Ala Arg Asp Asn Gly Trp Glu Leu Thr  
35 40 45  
Asp Trp Tyr Phe Asp Leu Trp Gly Arg Gly Thr Met Val Thr Val  
50 55 60  
Ser Ser  
62

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Asn Pro Ser Leu Lys Ser Arg Val Thr Ile Ser Val Asp Thr Ser  
1 5 10 15  
Lys Asn Gln Phe Ser Leu Lys Leu Ser Ser Val Thr Ala Ala Asp  
20 25 30  
Thr Ala Val Tyr Tyr Cys Ala Arg Val Asp Leu Glu Asp Tyr Gly  
35 40 45  
Ser Gly Ala Ser Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val  
50 55 60  
Ser Ser  
62

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 107 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Asp Ile Gln Met Thr Gln Ser Pro Ser Thr Leu Ser Ala Ser Ile  
1 5 10 15  
Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Glu Gly Ile Tyr  
20 25 30  
His Trp Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
35 40 45  
Leu Leu Ile Tyr Lys Ala Ser Ser Leu Ala Ser Gly Ala Pro Ser  
50 55 60  
Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
65 70 75  
Ser Ser Leu Gln Pro Asp Asp Phe Ala Thr Tyr Tyr Cys Gln Gln  
80 85 90

Tyr Ser Asn Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu Glu  
95 100 105

Ile Lys  
107

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Asn	Ala	Tyr	Ala	Leu	Lys	Met	Ala	Asp	Pro	Asn	Arg	Phe	Arg	Gly	1	5	10	15
Lys	Asp	Leu	Ala	Ala	His	Tyr	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	20	25	30	
Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	35	40	45	
Ser	Leu	Trp	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	50	55	60	
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	65	70	75	
Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	80	85	90	
Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	95	100	105	
Ser	Cys	Ser	Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	110	115	120	
Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	Lys	Xaa	Met	Lys	Lys	Asn	Ile	125	130	135	
Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	Ser	Ile	Ala	Thr	Asn	140	145	150	
Ala	Tyr	Ala	Gly	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	155	160	165	
Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Tyr	Cys	170	175	180	

Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu
				185					190					195
Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val
				200					205					210
Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Phe	Leu	Thr	Val
				215					220					225
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val
				230					235					240
Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser
				245					250					255
Leu	Ser	Pro	Gly	Lys	Xaa									
				260	261									